GEPHE SUMMARY

Gephebase Gene
ebony (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^ebony^#gephebase-summary-title)

GepheID
GP00000252

Entry Status
Published

Main curator
Courtier

PHENOTYPIC CHANGE

Trait Category
Morphology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Morphology^#gephebase-summary-title)

Trait
Coloration (posterior abdomen) (https://www.gephebase.org/search-criteria?/and+Trait=^Coloration (posterior abdomen)^#gephebase-summary-title)

Trait State in Taxon A
Drosophila melanogaster - Southern Japan; light

Trait State in Taxon B
Drosophila melanogaster - Southern Japan; dark

Ancestral State
Data not curated

Taxonomic Status
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Intraspecific^#gephebase-summary-title)

Taxon A

Latin Name
Drosophila melanogaster (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Drosophila melanogaster^#gephebase-summary-title)

Common Name
fruit fly

Synonyms
Sophophora melanogaster; fruit fly; Drosophila melanogaster Meigen, 1830; Sophophora melanogaster (Meigen, 1830); Drosophila melangaster

Rank
species

Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Diptera; Brachycera; Muscomorpha; Eremoneura; Cyclorrhapha; Schizophora; Acalyptratae; Ephydroidea; Drosophilidae; Drosophilinae; Drosophilini; Drosophila; Sophophora; melanogaster group; melanogaster subgroup

Parent
melanogaster subgroup () - (Rank: species subgroup) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 32351)

NCBI Taxonomy ID
7227 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7227)

is Taxon A an Infraspecies?
Yes

Taxon A Description
Drosophila melanogaster - Southern Japan; light

Taxon B

Latin Name
Drosophila melanogaster (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Drosophila melanogaster^#gephebase-summary-title)

Common Name
fruit fly

Synonyms
Sophophora melanogaster; fruit fly; Drosophila melanogaster Meigen, 1830; Sophophora melanogaster (Meigen, 1830); Drosophila melangaster

Rank
species

Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Diptera; Brachycera; Muscomorpha; Eremoneura; Cyclorrhapha; Schizophora; Acalyptratae; Ephydroidea; Drosophilidae; Drosophilinae; Drosophilini; Drosophila; Sophophora; melanogaster group; melanogaster subgroup

Parent
melanogaster subgroup () - (Rank: species subgroup) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 32351)

NCBI Taxonomy ID
7227 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7227)

is Taxon B an Infraspecies?
Yes

Taxon B Description
Drosophila melanogaster - Southern Japan; dark

GENOTYPIC CHANGE

Generic Gene Name
e

Synonyms
ebony; CG3331

String
-

Sequence Similarities
-

GO - Molecular Function
GO:0000036 : acyl carrier activity (https://www.ebi.ac.uk/QuickGO/term/GO:0000036)
GO:0003833 : beta-alanyl-dopamine synthase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003833)
GO:0031177 : phosphopantetheine binding

UniProtKB Drosophila melanogaster
O76858 (http://www.uniprot.org/uniprot/O76858)

GenebankID or UniProtKB
AJ224446 (https://www.ncbi.nlm.nih.gov/nuccore/AJ224446)

(https://www.ebi.ac.uk/QuickGO/term/GO:0031177)

GO - Biological Process

GO:0048085 : adult chitin-containing cuticle pigmentation
(https://www.ebi.ac.uk/QuickGO/term/GO:0048085)
GO:0042417 : dopamine metabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0042417)
GO:0007623 : circadian rhythm (https://www.ebi.ac.uk/QuickGO/term/GO:0007623)
GO:0048082 : regulation of adult chitin-containing cuticle pigmentation
(https://www.ebi.ac.uk/QuickGO/term/GO:0048082)
GO:0048066 : developmental pigmentation
(https://www.ebi.ac.uk/QuickGO/term/GO:0048066)
GO:0043042 : amino acid adenylylation by nonribosomal peptide synthase
(https://www.ebi.ac.uk/QuickGO/term/GO:0043042)
GO:0007593 : chitin-based cuticle sclerotization
(https://www.ebi.ac.uk/QuickGO/term/GO:0007593)
GO:0048067 : cuticle pigmentation (https://www.ebi.ac.uk/QuickGO/term/GO:0048067)
GO:0001692 : histamine metabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0001692)
GO:0045475 : locomotor rhythm (https://www.ebi.ac.uk/QuickGO/term/GO:0045475)
GO:0006583 : melanin biosynthetic process from tyrosine
(https://www.ebi.ac.uk/QuickGO/term/GO:0006583)
GO:0048022 : negative regulation of melanin biosynthetic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0048022)
GO:0042440 : pigment metabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0042440)

GO - Cellular Component

GO:0005737 : cytoplasm (https://www.ebi.ac.uk/QuickGO/term/GO:0005737)

Presumptive Null

No (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^No^#gephebase-summary-title)

Molecular Type

Cis-regulatory (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Cis-regulatory^#gephebase-summary-title)

Aberration Type

Unknown (https://www.gephebase.org/search-criteria?/and+Aberration Type=^Unknown^#gephebase-summary-title)

Molecular Details of the Mutation

17 nucleotide sites and 2 indels in complete association with the thoracic trident pigmentation intensity in a 13kb region

Experimental Evidence

Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Linkage Mapping^#gephebase-summary-title)

Main Reference

Divergent enhancer haplotype of ebony on inversion In(3R)Payne associated with pigmentation variation in a tropical population of Drosophila melanogaster. (2011)
(https://pubmed.ncbi.nlm.nih.gov/21914015)

Authors

Takahashi A; Takano-Shimizu T

Abstract

The pattern and intensity of pigmentation have direct impact on individual fitness through various ecological factors. In a Drosophila melanogaster population from southern Japan, thoracic trident pigmentation intensity of most of the strains could be classified into Dark or Light-type. The expression level variation of the ebony gene correlated well with this phenotype and the allelic differences in expression indicated that the variation is partly due to cis-regulatory changes. In the â^¼413â€ƒkb gene region, we identified 17 nucleotide sites and 2 indels that were in complete association with the thoracic trident pigmentation intensity. Interestingly, 11 out of 19 sites located within â^¼40.5â€ƒkb of the core epidermis enhancer. These sites had no obvious association with the abdominal pigmentation intensity in the previously analysed African populations from Uganda and Kenya, which suggested that multiple potential mutational pathways in the cis-regulatory control region of a single gene could lead to similar phenotypic variation within this species. We also found that the Light-type enhancer haplotype is strongly linked to a cosmopolitan inversion, In(3R)Payne, which is predominant in warmer climatic regions in both hemispheres. The sequence pattern suggested that the strong linkage may be due to selective forces related to thermal adaptation. The inferred selection for lighter pigmentation in the Japanese population is in the opposite direction of the previously reported case of selection for darker individuals in African populations. Nevertheless, both adaptive changes involved cis-regulatory changes of ebony, which shows that this gene is likely to be a common target of natural selection.

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Additional References

RELATED GEPHE

Related Genes

5 (bab, bab1, tan, yellow, wingless (wg)) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^7227^/and+Trait=Coloration/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

2 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^ebony^/and+Taxon ID=^7227^/or+Gene Gephebase=^ebony^/and+Taxon ID=^7227^#gephebase-summary-title)

EXTERNAL LINKS

COMMENTS

Contributions of each individual mutation was not tested